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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/762,594

DATE: 08/30/2001

TIME: 07:24:29

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3 <110> APPLICANT: PAPADOPoulos, VASSILIOS
4      HAU, LI
6 <120> TITLE OF INVENTION: PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR ASSOCIATED
7      PROTEINS, CLONING, EXPRESSION AND METHODS OF USE
9 <130> FILE REFERENCE: 082137-0277848
11 <140> CURRENT APPLICATION NUMBER: 09/762,594
12 <141> CURRENT FILING DATE: 2001-02-09
14 <150> PRIOR APPLICATION NUMBER: PCT/US99/18507
15 <151> PRIOR FILING DATE: 1999-08-11
17 <150> PRIOR APPLICATION NUMBER: 60/096,048
18 <151> PRIOR FILING DATE: 1998-08-11
20 <160> NUMBER OF SEQ ID NOS: 11
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25 <211> LENGTH: 505
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27 <213> ORGANISM: Mus musculus
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32 tcgtgccaag aaatggtcag aggaaataga aaatctgtac agatttcaac aagcaggata 180
33 tcgggatgaa attgaatata aacaagtgaa acaaggccatgatggtcgacc gatggccaga 240
34 gacagggtac gtgaagaaac ttca gggatggcggag ggacaataact ttcttctact acaacaaaga 300
35 gagggagtgcc gaggacaagg aggtccacaa agtgaaggtt tacgtctact gacctttcc 360
36 ttcttcggc ttggcaatgc tccttaaga attgggtt tacattcttc catcggtaa 420
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49 tc当地acttat gaagaaaac tgaagttcgat ggcactgcat aagcaagtcc ttttggccc 180
50 atataacccca gacacgtccc ctgagggttg attcttgcgt gtgtggggat atgataggag 240
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54 acgagagcgg ctgcaaaagg aagaagagaa gcgaaagcga gaggaggaaacccgctgag 480
55 acgggaggag gaagagaggc ggcggataga ggaagagagg cttcggctgg aacagcaaaa 540
56 gcagcagata atggcagctt taaactcgca gactgccgtg caattccagc agtatgcagc 600
57 ccagcagtat ccagggaaact acgaacaaca gcagattctc atccgccagc tgcaggagca 660
58 gcactatcag cagtataaac accaggcaga gcaaacccaa cctgcacaac aacaggcagc 720
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62 agactcttccaggatttggacatgtggacaagaccacaaa tcaaagactt 960
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 64 caccgtccga gtccccactcatgaggaaggatcataccta ttttggaaat ttgccacaga 1080
 65 cagttatgac attgggttttgggttattttgaatggaca gactctccaa atgctgtgt 1140
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 104 cggctgttttccgacaaccatcagagccagacccatcacaagccatggatggatgg 420
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 117 tccagtgccatcaaaatactaaaggccaaa gaaacaagagaaatctccatgtatgt 180
 118 ctcacagtc当地ggccaccatcggatggatggatggatggatggatggatgg 240
 119 agccgtcgaaataccagaaagcagctccaaacctgccc当地aaaggaaatttcttacatct 300

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120 tcaatcgaaa atttcatcag atggccaaaa agatggactt aacctaagta catctcaaca 360
 121 agaaaagtatt tcaatgattc ctaaagggtcc tcctgaaaac tcagttatca gctgtgactc 420
 122 ccaggcccta aatatgttag ctgatctggc attaaggctc gctgctgctt ctataaccatc 480
 123 ttgtaagccc aggaaccttc cctgcgtctc tgattgcca ccaaacaatg tcttactcac 540
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 128 <211> LENGTH: 88
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 133 Met Ala Thr Ser Asp Val Lys Pro Lys Ser Ile Ser Arg Ala Lys Lys
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 136 Trp Ser Glu Glu Ile Glu Asn Leu Tyr Arg Phe Gln Gln Ala Gly Tyr
 137 20 25 30
 139 Arg Asp Glu Ile Glu Tyr Lys Gln Val Lys Gln Val Ala Met Val Asp
 140 35 40 45
 142 Arg Trp Pro Glu Thr Gly Tyr Val Lys Lys Leu Gln Arg Arg Asp Asn
 143 50 55 60
 145 Thr Phe Phe Tyr Tyr Asn Lys Glu Arg Glu Cys Glu Asp Lys Glu Val
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 161 Lys Val Val Leu Phe Leu Asn Gln Leu Ser Leu Cys Lys Leu Val Lys
 162 20 25 30
 164 Asp Gly Lys Ala Phe His Pro Thr Tyr Glu Glu Lys Leu Lys Phe Val
 165 35 40 45
 167 Ala Leu His Lys Gln Val Leu Leu Gly Pro Tyr Asn Pro Asp Thr Ser
 168 50 55 60
 170 Pro Glu Val Gly Phe Phe Asp Val Leu Gly Asn Asp Arg Arg Arg Glu
 171 65 70 75 80
 173 Trp Ala Ala Leu Gly Asn Met Ser Lys Glu Asp Ala Met Val Glu Phe
 174 85 90 95
 176 Val Lys Leu Leu Asn Lys Cys Cys Pro Leu Leu Ser Ala Tyr Val Ala
 177 100 105 110
 179 Ser His Arg Ile Glu Lys Glu Glu Glu Lys Arg Arg Lys Ala Glu
 180 115 120 125
 182 Glu Glu Arg Arg Gln Arg Glu Glu Glu Arg Glu Arg Leu Gln Lys
 183 130 135 140
 185 Glu Glu Glu Lys Arg Lys Arg Glu Glu Glu Asp Arg Leu Arg Arg Glu
 186 145 150 155 160
 188 Glu Glu Glu Arg Arg Ile Glu Glu Glu Arg Leu Arg Leu Glu Gln
 189 165 170 175

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191 Gln Lys Gln Gln Ile Met Ala Ala Leu Asn Ser Gln Thr Ala Val Gln
 192 180 185 190
 194 Phe Gln Gln Tyr Ala Ala Gln Gln Tyr Pro Gly Asn Tyr Glu Gln Gln
 195 195 200 205
 197 Gln Ile Leu Ile Arg Gln Leu Gln Glu Gln His Tyr Gln Gln Tyr Lys
 198 210 215 220
 200 His Gln Ala Glu Gln Thr Gln Pro Ala Gln Gln Ala Ala Leu Gln
 201 225 230 235 240
 203 Lys Gln Gln Glu Val Val Met Ala Gly Ala Ser Leu Pro Ala Ser Ser
 204 245 250 255
 206 Lys Val Asn Thr Ala Gly Ala Ser Asp Thr Leu Ser Val Asn Gly Gln
 207 260 265 270
 209 Ala Lys Thr His Thr Glu Asn Ser Glu Lys Val Leu Glu Pro Glu Ala
 210 275 280 285
 212 Ala Glu Glu Ala Leu Glu Asn Gly Pro Lys Asp Ser Leu Pro Val Ile
 213 290 295 300
 215 Ala Ala Pro Ser Met Trp Thr Arg Pro Gln Ile Lys Asp Phe Lys Glu
 216 305 310 315 320
 218 Lys Ile Arg Gln Asp Ala Asp Ser Val Ile Thr Val Arg Arg Gly Glu
 219 325 330 335
 221 Val Val Thr Val Arg Val Pro Thr His Glu Glu Gly Ser Tyr Leu Phe
 222 340 345 350
 224 Trp Glu Phe Ala Thr Asp Ser Tyr Asp Ile Gly Phe Gly Val Tyr Phe
 225 355 360 365
 227 Glu Trp Thr Asp Ser Pro Asn Ala Ala Val Ser Val His Val Ser Glu
 228 370 375 380
 230 Ser Ser Asp Glu Glu Glu Glu Glu Glu Asn Val Thr Cys Glu Glu
 231 385 390 395 400
 233 Lys Ala Lys Lys Asn Ala Asn Lys Pro Leu Leu Asp Glu Ile Val Pro
 234 405 410 415
 236 Val Tyr Arg Arg Asp Cys His Glu Glu Val Tyr Ala Gly Ser His Gln
 237 420 425 430
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 242 Leu Trp Arg Ser Lys Ser Val Tyr Tyr Arg Val Tyr Tyr Thr Arg
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 247 <211> LENGTH: 158
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 256 20 25 30
 258 Thr Trp Gln Ser Ser Glu Ser Ser Gln Ser Asn Leu Gly Glu Gln Thr
 259 35 40 45
 261 Gln Ser Gly Pro Gln Gly Gly Arg Cys Gln Arg Arg Glu Arg His Asn
 262 50 55 60

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264 Arg Met Glu Arg Asp Arg Arg Arg Arg Ile Arg Ile Cys Cys Asp Glu
265 65 70 75 80
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268 85 90 95
270 Thr Leu Gln Trp Thr Thr Ala Phe Leu Lys Tyr Ile Gln Glu Arg His
271 100 105 110
273 Gly Asp Ser Leu Lys Lys Glu Phe Glu Ser Val Phe Cys Gly Lys Thr
274 115 120 125
276 Gly Arg Arg Leu Lys Leu Thr Arg Pro Glu Ser Leu Val Thr Cys Pro
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295 Ser Pro Arg Pro Glu His Val Pro Cys Gly Thr Cys Ser Val Thr Ala
296 35 40 45
298 Glu Pro Ala Gln Pro Ala Phe Leu Lys Leu Gly Val Ser Cys Pro Gln
299 50 55 60
301 Pro Ser Gln Gln Ser Val Cys Phe Pro Thr Thr Ser Glu Pro Asp Leu
302 65 70 75 80
304 Thr Ser Leu Phe Trp Trp Phe Pro Lys Phe Leu Ser Asp Leu His Val
305 85 90 95
307 Tyr Pro Ser Thr Pro Ser Lys Arg Glu Arg Lys Glu Leu Arg Lys Lys
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313 <211> LENGTH: 196
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324 Glu Ala Ser Val Ser Lys Asp Ala Pro Val Pro Thr Asn Thr Lys Arg
325 35 40 45
327 Ala Lys Lys Gln Glu Lys Ser Pro Gly Arg Ile Ala Ser Gln Ser Lys
328 50 55 60
330 Pro Pro Met Lys Lys Ser Pro Gln Lys Arg Lys Val Asn Val Ala Arg
331 65 70 75 80
333 Gly Arg Arg Asn Thr Arg Lys Gln Leu Gln Pro Ala Glu Lys Glu Ile
334 85 90 95
336 Ala Leu His Leu Gln Ser Glu Ile Ser Ser Asp Gly Gln Lys Asp Gly

VERIFICATION SUMMARY

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